

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 21, 2001, 12:07:03 ; Search time 22.69 Seconds  
(without alignments)  
1830.929 Million cell updates/sec

Title: US-09-486-334-2  
Perfect score: 1641  
Sequence: 1 MATCIDRCRGNTQDDSRF.....IPCLTMDQSYLWSDYVI 314

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP-REMBL-16:\*  
2: SP-archaea:\*  
3: SP-bacteria:\*  
4: SP-fungi:\*  
5: SP-human:\*  
6: SP-invertebrate:\*  
7: SP-mammal:\*  
8: SP-mhc:\*  
9: SP-organelle:\*  
10: SP-phage:\*  
11: SP-plant:\*  
12: SP-rodent:\*  
13: SP-unclassified:\*  
14: SP-vertebrate:\*  
15: SP-virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1641	100.0	314	10	043297
2	1611	98.2	314	10	042588
3	1215	74.0	391	10	042532
4	1208	73.6	336	10	039218
5	877	53.4	347	10	093544
6	872	53.1	289	10	09MAZ3
7	869	53.0	294	10	09SDP2
8	861	52.5	289	10	09SDP2
9	849.5	51.8	323	10	09STB0
10	711	43.3	368	10	09STB0
11	699	42.6	315	10	09STB6
12	649.5	39.6	272	2	09JRB6
13	647.5	39.5	273	2	09JRB6
14	629.5	38.4	402	10	09SLZ8
15	610.5	37.2	312	2	09L3R1
16	587.5	35.8	299	10	081795
17	472.5	28.8	270	3	09US33
18	472.5	28.8	270	3	09US33
19	422.5	25.7	227	2	032979

20	415.5	25.3	245	2	086162	086162 synechococ
21	409	24.9	251	2	069218	069218 azobacter
22	405	24.7	229	2	P95231	P95231 mycobacteri
23	395	24.1	229	2	09KGF5	09KGF5 bacillus ha
24	392	23.9	258	2	09HX16	09HX16 pseudomonas
25	391	23.8	243	1	09HNA4	09HNA4 methanosarc
26	388.5	23.7	212	2	09PPF6	09PPF6 campylobact
27	378	23.0	191	2	09LAR1	09LAR1 clostridium
28	370	22.5	265	2	044541	044541 azobacter
29	338.5	20.6	220	2	09WZD4	09WZD4 thermotoga
30	312	19.0	171	1	09HPT3	09HPT3 halobacteri
31	307.5	18.7	305	5	09UBX2	09UBX2 entamoeba h
32	298	18.2	439	10	09M9F2	09M9F2 arbidopsi
33	290	17.7	300	5	09UBX0	09UBX0 entamoeba d
34	287	17.5	305	5	09UBX1	09UBX1 entamoeba d
35	265	16.1	231	2	09I210	09I210 pseudomonas
36	263	16.1	162	2	09F7A9	09F7A9 salmonella
37	207	13.0	184	2	09KTI3	09KTI3 vibrio chol
38	204	12.4	197	2	09SV13	09SV13 escherichia
39	193	11.8	275	5	09CV13	09CV13 leishmania
40	184.5	11.2	419	2	09RDX7	09RDX7 legionella
41	177.5	10.8	143	2	09KTH9	09KTH9 thermotoga
42	175	10.7	236	2	09XIK7	09XIK7 bacillus ha
43	175	10.7	240	2	09K9H8	09K9H8 bacillus ha
44	168	10.2	172	2	09XAC2	09XAC2 escherichia
45	162.5	9.9	239	2	09EZ10	09EZ10 staphylococ

## ALIGNMENTS

RESULT 1  
043297 043297 PRELIMINARY; PRT; 314 AA.  
AC 043297;  
DE 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)  
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)  
DE (P14J16.18).  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX MEDLINE=95154333; PubMed=7851429;  
RA Ruffet M.L., Lebun M., Droux M., Douce R.;  
RT "Subcellular distribution of serine acetyltransferase from Pisum  
RT sativum and characterization of an Arabidopsis thaliana putative  
RT cytosolic isoform";  
RL Eur. J. Biochem. 227:500-509(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX Ruffet M.L., Lebun M., Droux M., Douce R.;  
RA Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,  
RA Kim C., Alfieri H., Bel O., Chin C., Chou J., Choi E., Conn L.,  
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,  
RA Lanz C., Li J., Liu K., Liu S., Mukhin N., Nguyen M.,  
RA Palm C., Pham P., Sakano H., Schwartz J., Soulikov A., Thayer A.,  
RA Toriumi M., Vaynsberg M., Yu G., Federspiel N.A., Theologis A.,  
RA Ecker J.R.;  
RT "Genomic sequence for Arabidopsis thaliana BAC F14J16 from chromosome  
RT 1";  
RN Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.

RA Ecker J.R.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chlou J., Choi E.,  
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharly N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Thayer A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 RA Theologis A., Ecker J.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-  
 CC SERINE.  
 DR EMBL: Z34888; CA84371.1; -;  
 DR EMBL: L34076; AA58608.1; -;  
 DR EMBL: AC002304; AA79319.1; -;  
 DR Mendel: 6701; At4th:1221;6701.  
 DR InterPro: IPR001451; -;  
 DR Pfam: PF00132; hexapet: 3.  
 DR PROSITE: PS00101; HEXAPEP\_TRANSFERRASES: 1.  
 DR TRANSFERRASE; Acyltransferase.  
 SQ SEQUENCE 314 AA; 34251 MW; 78ACE3DA5CE04B0 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 1641; DB 10; Length 314;  
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MATCIDTCRGNTODDDSRCCIKNFRRGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60  
 DB 1 MATCIDTCRGNTODDDSRCCIKNFRRGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60  
 OY 61 KQPIILSNYYASITSHRSLSALAHILSVKLSNLPNSNLFELFISVEESPETIEST 120  
 DB 61 KQPIILSNYYASITSHRSLSALAHILSVKLSNLPNSNLFELFISVEESPETIEST 120  
 OY 121 KODLIAVKEPDPACTSYVHCFGLGKFLACQAHRIATHTLKNRKIVALLIONRVSESA 180  
 DB 121 KODLIAVKEPDPACTSYVHCFGLGKFLACQAHRIATHTLKNRKIVALLIONRVSESA 180  
 OY 181 VDIHPGAKIGKILIDHATGVVIGETAVGDNVSIHGVTLGGTGKSGDRPKIGDYL 240  
 DB 181 VDIHPGAKIGKILIDHATGVVIGETAVGDNVSIHGVTLGGTGKSGDRPKIGDYL 240  
 OY 241 IGAGSCIIGNTTIGGAKIGSGSVYVNDVARTAVGNPARKLIGKENPRKHDKIPCLTM 300  
 DB 241 IGAGSCIIGNTTIGGAKIGSGSVYVNDVARTAVGNPARKLIGKENPRKHDKIPCLTM 300  
 OY 301 DOTSYLTWMSDYVI 314  
 DB 301 DOTSYLTWMSDYVI 314  
 ID 042588 PRELIMINARY; PRT; 314 AA.  
 AC 042588;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)

DE SERINE ACETYLTANSFERASE (EC 2.3.1.30) (SERIII, O-ACETYLTANSFERASE).  
 OS Arabidopsis thaliana (mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_Taxid=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Murillo M., Foglia R., Diller A., Leustek T.;  
 RL Cell. Mol. Biol. Res. 0:0-0(0).  
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-  
 CC SERINE.  
 DR EMBL: L42212; AAC37474.1; -;  
 DR Mendel: 6700; At4th:1221;6700.  
 DR InterPro: IPR001451; -;  
 DR Pfam: PF00132; hexapet: 3.  
 DR PROSITE: PS00101; HEXAPEP\_TRANSFERRASES: 1.  
 DR TRANSFERRASE; Acyltransferase.  
 SQ SEQUENCE 314 AA; 34259 MW; A096DF6D2768E21C CRC64;

Query Match  
 Best Local Similarity 98.2%; Score 1611; DB 10; Length 314;  
 Matches 308; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 MATCIDTCRGNTODDDSRCCIKNFRRGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60  
 DB 1 MATCIDTCRGNTODDDSRCCIKNFRRGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60  
 OY 61 KQPIILSNYYASITSHRSLSALAHILSVKLSNLPNSNLFELFISVEESPETIEST 120  
 DB 61 KQPIILSNYYASITSHRSLSALAHILSVKLSNLPNSNLFELFISVEESPETIEST 120  
 OY 121 KODLIAVKEPDPACTSYVHCFGLGKFLACQAHRIATHTLKNRKIVALLIONRVSESA 180  
 DB 121 KODLIAVKEPDPACTSYVHCFGLGKFLACQAHRIATHTLKNRKIVALLIONRVSESA 180  
 OY 181 VDIHPGAKIGKILIDHATGVVIGETAVGDNVSIHGVTLGGTGKSGDRPKIGDYL 240  
 DB 181 VDIHPGAKIGKILIDHATGVVIGETAVGDNVSIHGVTLGGTGKSGDRPKIGDYL 240  
 OY 241 IGAGSCIIGNTTIGGAKIGSGSVYVNDVARTAVGNPARKLIGKENPRKHDKIPCLTM 300  
 DB 241 IGAGSCIIGNTTIGGAKIGSGSVYVNDVARTAVGNPARKLIGKENPRKHDKIPCLTM 300  
 OY 301 DOTSYLTWMSDYVI 314  
 DB 301 DOTSYLTWMSDYVI 314

RESULT 3  
 ID 042532 PRELIMINARY; PRT; 391 AA.  
 AC 042532; 043740; Q43739;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
 DE SERINE ACETYLTANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTANSFERASE)  
 GN SMT-1 OR SAT1 OR SAT A.  
 OS Arabidopsis thaliana (mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_Taxid=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA MEDLINE=96270381; PubMed=8639741;  
 RA Roberts M.A., Wray J.L.;  
 RT "Cloning and characterization of an Arabidopsis thaliana cDNA clone  
 encoding an organellar isoform of serine acetyltransferase.";

Plant Mol. Biol. 30:1041-1049(1996).

12]

SEQUENCE OF 80-391 FROM N.A.

STRAIN-CV. COLUMBIA; TISSUE-LEAF;

MEDLINE:93121457; PubMed:7821427;

Bogdanova N., Bork C., Hell R.,

"Cysteine biosynthesis in plants: isolation and functional

identification of a cDNA encoding a serine acetyltransferase from

Arabidopsis thaliana."

FEBS Lett. 358:43-47(1995).

13]

SEQUENCE OF 56-391 FROM N.A.

STRAIN-CV. COLUMBIA; TISSUE-LEAF;

Hell R., Bogdanova N.;

Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.

14]

SEQUENCE FROM N.A.

STRAIN-COLUMBIA;

Kaneko T., Kato S., Nakamura Y., Asamizu E., Tabata S.;

Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

15]

SEQUENCE FROM N.A.

STRAIN-COLUMBIA;

PubMed:10907853;

Nakamura Y.;

"Structural analysis of Arabidopsis thaliana chromosome 3. II.

Sequence features of the regions of 4,251,695 bp covered by ninety pl,

TAC and BAC clones."

DNA Res. 7:217-221(2000).

1- CATALYTIC ACTIVITY: ACETYL-CoA + L-SERINE = CoA + O-ACETYL-L-

SERINE.

EMBL: U22964; AAB07778.1;

EMBL: X82888; CA58061.1;

EMBL: X80938; CA56913.1;

EMBL: AP000375; BAB01402.1;

Mendel; 6697; Arabid;1221:6698.

InterPro: IPR001451;

Pfam: PF00132; hexapep; 3.

PROSITE: PS00101; HEXAPEP\_TRANSFERRASES; 1.

TRANSFERASE: Acyltransferase.

SEQUENCE 391 AA; 42720 MW; A3ED09DEA53C10E2 CRC64;

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039218 PRELIMINARY; PRT: 336 AA.

ID 039218

AC 039218; 1996 (Trembl, 01, Created)

DT 01-NOV-1996 (Trembl, 01, Last sequence update)

DT 01-NOV-1996 (Trembl, 01, Last sequence update)

DT 01-OCT-2000 (Trembl, 15, Last annotation update)

DE SERINE ACETYLTRANSFERASE.

GN SATI.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Eudicotyledons; Core eudicots; rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsis.

OC NCBITaxID=3702;

OX [1]

SEQUENCE FROM N.A.

Ruffier M.L., Lebrun M., Droux M., Douce R.;

Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

EMBL: L78443; AAB02050.1;

Mendel; 6697; Arabid;1221:6697.

InterPro: IPR001451;

Pfam: PF00132; hexapep; 3.

PROSITE: PS00101; HEXAPEP\_TRANSFERRASES; 1.

TRANSFERASE

SEQUENCE 336 AA; 36454 MW; 331671D613434306 CRC64;

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039218 PRELIMINARY; PRT: 336 AA.

ID 039218

AC 039218; 1996 (Trembl, 01, Created)

DT 01-NOV-1996 (Trembl, 01, Last sequence update)

DT 01-NOV-1996 (Trembl, 01, Last sequence update)

DT 01-OCT-2000 (Trembl, 15, Last annotation update)

DE SERINE ACETYLTRANSFERASE.

GN SATI.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Eudicotyledons; Core eudicots; rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsis.

OC NCBITaxID=3702;

OX [1]

SEQUENCE FROM N.A.

Ruffier M.L., Lebrun M., Droux M., Douce R.;

Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

EMBL: L78443; AAB02050.1;

Mendel; 6697; Arabid;1221:6697.

InterPro: IPR001451;

Pfam: PF00132; hexapep; 3.

PROSITE: PS00101; HEXAPEP\_TRANSFERRASES; 1.

TRANSFERASE

SEQUENCE 336 AA; 36454 MW; 331671D613434306 CRC64;

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039218 PRELIMINARY; PRT: 336 AA.

ID 039218

AC 039218; 1996 (Trembl, 01, Created)

DT 01-NOV-1996 (Trembl, 01, Last sequence update)

DT 01-NOV-1996 (Trembl, 01, Last sequence update)

DT 01-OCT-2000 (Trembl, 15, Last annotation update)

DE SERINE ACETYLTRANSFERASE.

GN SATI.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Eudicotyledons; Core eudicots; rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsis.

OC NCBITaxID=3702;

OX [1]

SEQUENCE FROM N.A.

Ruffier M.L., Lebrun M., Droux M., Douce R.;

Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

EMBL: L78443; AAB02050.1;

Mendel; 6697; Arabid;1221:6697.

InterPro: IPR001451;

Pfam: PF00132; hexapep; 3.

PROSITE: PS00101; HEXAPEP\_TRANSFERRASES; 1.

TRANSFERASE



OY 217 HCVLLGTGKOSGDRHPIKIDGVILGAGSCILGNITIGGAKIGSGVYKDVPAATVAV 276  
 DB 197 HHTVLGGGKMGKGRHPIKIDGVILGAGATILGNVIGGAKIGAGSVVLIDVPPRTTAV 256  
 OY 277 GNPALVGGKMKHPIKIDGVILGAGATILGNVIGGAKIGAGSVVLIDVPPRTTAV 314  
 DB 257 GNPALVGGKMKHPIKIDGVILGAGATILGNVIGGAKIGAGSVVLIDVPPRTTAV 294

## RESULT 8

09SDP2 PRELIMINARY; PRT: 289 AA.

AC 09SDP2: 01-MAY-2000 (TREMUREL. 13, Created)  
 DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMUREL. 14, Last annotation update)  
 DE SERINE ACETYLTRANSFERASE.  
 OS Allium cepa (Onion).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.  
 OX NCBI\_TaxID=4679;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. PUKOHE LONG KEEPER; TISSUE=ROOT;  
 RA Pither-Joyce M.D., McCallum J.A.;  
 RT "Isolation of a serine acetyltransferase cDNA clone from Allium  
 cepa."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AF212156; AAF19000.1;  
 DR InterPro: IPR001451;  
 DR Pfam: PF00132; hexapep. 3.  
 DR PROSITE: PS00101; HEXAPEP\_TRANSFERASES; 1.  
 KW Transferrase.  
 SQ SEQUENCE 289 AA; 30574 MW; 9EA376C54DA0AF13 CRC64;

Query Match 52.5%; Score 861; DB 10; Length 289;  
 Best Local Similarity 59.8%; Pred. No. 4,4e-62;  
 Matches 162; Conservative 46; Mismatches 63; Indels 0; Gaps 0;

OY 44 DDDVWIKMEKSDVKOEPLISNYYASTSHRSLSALAHILSVLSMLNPSTLFL 103  
 DB 19 DESWVNOIKAEHRAESEPALASTYSTISHPSLARSLSFHLANLCSSTLSTLY 78  
 OY 104 ELFISVLESPEIESTKODLAVKREDPACISYHCEFGELACQAHIAHTLMKON 163  
 DB 79 DFLNLTSTFFVYLSASVADLIARNDPACISYHCEFGELACQAHIAHTLMKON 138  
 OY 164 RKTVALIONRVSEPAVDIHGPAKIGKILLDHATGVYIGETAVGDNVSLHCVTLGG 223  
 DB 139 RRLALALHSRVADVLSVADLIARNDPACISYHCEFGELACQAHIAHTLMKON 198  
 OY 224 TKGOSGDHRIKIDGVILGAGSCILGNITIGGAKIGSGVYKDVPAATVAV 283  
 DB 199 TGRAGGDRHPIKIDGVILGAGATILGNVIGGAKIGAGSVVLIDVPPRTTAV 258  
 OY 284 GKENPRKHDKIPCLTMDQTSYLTMSDYVI 314  
 DB 259 GKEKPSVHEDVPGESMDHTSFISEMSDYII 289

## RESULT 9

042538 PRELIMINARY; PRT: 312 AA.

AC 042538: 01-NOV-1996 (TREMUREL. 01, Created)  
 DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMUREL. 16, Last annotation update)  
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)  
 DE SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) (SAT-52).  
 GN SAT-52.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=97201050; PubMed=9048879;  
 RA Howarth J.R., Roberts M.A., Wray J.L.;  
 RT "Cysteine biosynthesis in higher plants: a new member of the  
 Arabidopsis thaliana serine acetyltransferase small gene family  
 obtained by functional complementation of an Escherichia coli cysteine  
 auxotroph."  
 RT auxotroph.  
 RL Biochim. Biophys. Acta 1350:123-127 (1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=98403884; PubMed=9734815;  
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.  
 RT Sequence features of the regions of 1,367,185 bp covered by 19  
 RT physically assigned P1 and PAC clones."  
 RL DNA Res. 5:203-216 (1998).  
 DR EMBL: U30298; AAC49655.1;  
 DR EMBL: AB013392; BAB09894.1;  
 DR Mendel: 6699; Arath:1221.6699.  
 DR InterPro: IPR001451;  
 DR Pfam: PF00132; hexapep. 3.  
 DR PROSITE: PS00101; HEXAPEP\_TRANSFERASES; 1.  
 KW Transferrase; Acyltransferase.  
 SQ SEQUENCE 312 AA; 32770 MW; 15835510FF314A3 CRC64;

Query Match 51.8%; Score 849.5; DB 10; Length 312;  
 Best Local Similarity 59.7%; Pred. No. 4.2e-61;  
 Matches 160; Conservative 45; Mismatches 62; Indels 1; Gaps 1;

OY 48 VWIKMEKSDVKOEPLISNYYASTSHRSLSALAHILSVLSMLNPSTLFL 107  
 DB 45 LMTOLKAEHRAESEPALASTYSTISHPSLARSLSFHLANLCSSTLSTLY 104  
 OY 108 ELFISVLESPEIESTKODLAVKREDPACISYHCEFGELACQAHIAHTLMKON 167  
 DB 105 NTFSSPDLRNATVADLIARNDPACISYHCEFGELACQAHIAHTLMKON 164  
 OY 168 ALLIONRVSEPAVDIHGPAKIGKILLDHATGVYIGETAVGDNVSLHCVTLGG 227  
 DB 165 ALALHSRISDVADVLIARNDPACISYHCEFGELACQAHIAHTLMKON 224  
 OY 228 SGDRHPIKIDGVILGAGSCILGNITIGGAKIGSGVYKDVPAATVAV 287  
 DB 225 GDRHPIKIDGVILGAGATILGNVIGGAKIGAGSVVLIDVPPRTTAV 284  
 OY 288 NPKRHD-KIPCLTMDQTSYLTMSDYVI 314  
 DB 285 KPTIHDECPGEGMDHTSFISEMSDYII 312

## RESULT 10

092PJ4 PRELIMINARY; PRT: 323 AA.

AC 092PJ4: 01-MAY-1999 (TREMUREL. 10, Created)  
 DT 01-MAY-1999 (TREMUREL. 10, Last sequence update)  
 DT 01-MAY-2000 (TREMUREL. 13, Last annotation update)  
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30).  
 GN SAT-106.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Howarth J.R., Roberts M.A., Wray J.L.;  
RT "A fourth member of the serine acetyltransferase gene-family from  
RL Arabidopsis thaliana.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF112303; AAD19965.1;  
DR InterPro: IPR001451;  
DR Pfam: PF00132; hexaped; 2.  
DR PROSITE: PS00101; HEXAPEP\_TRANSFERASES; 1.  
DR Transferrase: Acyltransferase.  
SQ SEQUENCE 323 AA; 34534 MM; 8CE538962B44E610 CRC64;

Query Match 43.3%; Score 711; DB 10; Length 323;  
Best Local Similarity 50.5%; Pred. No. 7,7e-50;  
Matches 141; Conservative 48; Mismatches 78; Indels 12; Gaps 3;

QY 27 FRPGSVNKK-IHHTQIEDD-----DDWIKMLEAKSDVKQEPILSNYYASTSHRS 79  
DB 8 FESGEVYAKGTHKSEFDSNLDPRSDPIWDAIREAKLEAEKPEILSFLYAGILAHDC 67  
QY 80 LESALAHILSVKLSNLDNPSNTLFEFISYLEESPETIEESTKODLIIVKRDPACTSYH 139  
DB 68 LEQALGFVLANKLQNPITLALQGLDIFGVMMHDKGIQSSIRHDLQAFKDRDPACLSYS 127  
QY 140 CFLGKGFACQAHRIAHITLTKQNRKIYALLIQRVSESPAVNDIHPGAKIGKILLDHAT 199  
DB 128 AILHLKGYHALQAVYAVHAKLNMEGRKLLALQSRISVEGIDIHPARIGEGILLDHGT 187  
QY 200 GVIGETAVNGDVSILHGVTLGSTGKSGDRHPRKIGDGVILGAGSCILGNTITGCAKI 259  
DB 188 GVIGETAVNGVSILHGVTLGSTGKSGDRHPRKIGEGALACVTLIGNISIGAGAMV 247  
QY 260 GGSVYVAVKDPARTTAVGNPARLIGKEN-----PRKHD 293  
DB 248 AAGSLVLKDVPSHVSVAQNPALKIRWEEDPPLAMKHD 286

RESULT 11  
Q9STB0 ID Q9STB0 PRELIMINARY; PRT; 368 AA.  
AC Q9STB0;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)  
DE SERINE ACETYLTRANSFERASE 2.  
GN SAT2.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxId=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Ruffet M.-L., Lebun M., Droux M., Douce R.;  
RT "Gene sequence of serine acetyltransferase 2 from A. thaliana.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: L78444; AAD5614.2;  
DR InterPro: IPR001451;  
DR Pfam: PF00132; hexaped; 2.  
DR PROSITE: PS00101; HEXAPEP\_TRANSFERASES; 1.  
SQ SEQUENCE 368 AA; 39575 MM; 84BC097D15FCASCE CRC64;

Query Match 43.3%; Score 711; DB 10; Length 368;  
Best Local Similarity 50.5%; Pred. No. 9,3e-50;  
Matches 141; Conservative 48; Mismatches 78; Indels 12; Gaps 3;  
QY 27 FRPGSVNKK-IHHTQIEDD-----DDWIKMLEAKSDVKQEPILSNYYASTSHRS 79  
DB 53 FESGEVYAKGTHKSEFDSNLDPRSDPIWDAIREAKLEAEKPEILSFLYAGILAHDC 112

QY 80 LESALAHILSVKLSNLDNPSNTLFEFISYLEESPETIEESTKODLIIVKRDPACTSYH 139  
DB 113 LEQALGFVLANKLQNPITLALQGLDIFGVMMHDKGIQSSIRHDLQAFKDRDPACLSYS 172  
QY 140 CFLGKGFACQAHRIAHITLTKQNRKIYALLIQRVSESPAVNDIHPGAKIGKILLDHAT 199  
DB 173 AILHLKGYHALQAVYAVHAKLNMEGRKLLALQSRISVEGIDIHPARIGEGILLDHGT 232  
QY 200 GVIGETAVNGDVSILHGVTLGSTGKSGDRHPRKIGDGVILGAGSCILGNTITGCAKI 259  
DB 233 GVIGETAVNGVSILHGVTLGSTGKSGDRHPRKIGEGALACVTLIGNISIGAGAMV 292  
QY 260 GGSVYVAVKDPARTTAVGNPARLIGKEN-----PRKHD 293  
DB 293 AAGSLVLKDVPSHVSVAQNPALKIRWEEDPPLAMKHD 331

RESULT 12  
Q9SEY6 ID Q9SEY6 PRELIMINARY; PRT; 315 AA.  
AC Q9SEY6;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)  
DE PUTATIVE SERINE ACETYLTRANSFERASE.  
GN ATG17640.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxId=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA MEDLINE=20083487; PubMed=10617197;  
RA Lin X., Kaul S., Rounsley S.D., Buehler T.P., Beilstein M., Town C.D.,  
RA Buell C.R., Mason T.M., Bowman C.L., Barnstaele M.E., Feldblyum T.V.,  
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Pailon L.J., Gill J.E.,  
RA Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
RA Salzberg S.L., Fraser C.M., Ventner J.C.;  
RT "Sequence and analysis of chromosome II of Arabidopsis thaliana.";  
RL Nature 402:761-768(1999).  
DR EMBL: AF024504; AF18673.1;  
DR InterPro: IPR001451;  
DR Pfam: PF00132; hexaped; 2.  
DR PROSITE: PS00101; HEXAPEP\_TRANSFERASES; 1.  
DR Transferrase.  
SQ SEQUENCE 315 AA; 34000 MM; FD15AC3E8A150B2E CRC64;

Query Match 42.6%; Score 699; DB 10; Length 315;  
Best Local Similarity 50.2%; Pred. No. 7e-49;  
Matches 141; Conservative 50; Mismatches 76; Indels 14; Gaps 4;  
QY 27 FRPGSVNKK-IHHTQIEDD-----DDWIKMLEAKSDVKQEPILSNYYASTSHRS 79  
DB 8 FESGEVYAKGTHKSEFDSNLDPRSDPIWDAIREAKLEAEKPEILSFLYAGILAHDC 65  
QY 80 LESALAHILSVKLSNLDNPSNTLFEFISYLEESPETIEESTKODLIIVKRDPACTSYH 139  
DB 66 LEQALGFVLANKLQNPITLALQGLDIFGVMMHDKGIQSSIRHDLQAFKDRDPACLSYS 125  
QY 140 CFLGKGFACQAHRIAHITLTKQNRKIYALLIQRVSESPAVNDIHPGAKIGKILLDHAT 199  
DB 126 AILHLKGYHALQAVYAVHAKLNMEGRKLLALQSRISVEGIDIHPARIGEGILLDHGT 185  
QY 200 GVIGETAVNGDVSILHGVTLGSTGKSGDRHPRKIGDGVILGAGSCILGNTITGCAKI 259  
DB 186 GVIGETAVNGVSILHGVTLGSTGKSGDRHPRKIGEGALACVTLIGNISIGAGAMV 245

OY 260 GSGSVVYKVPARTAVGNPARRLIGKSNPRKHXIPCLTM 300  
 :||:||||: : ||||:| : :||:|  
 Db 246 AAGSLVAKDPHSHSVYAGNPAKLIRYME-----EDDPSLAM 281

## RESULT 13

09JUR86 PRELIMINARY: PRT: 272 AA.  
 AC 09JUR86;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
 DE PUTATIVE SERINE ACETYLTRANSFERASE (EC 2.3.1.30).  
 GN CSE OR NMA0742 OR NMB0560.  
 OS Neisseria meningitidis (serogroup A), and  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=65699, 491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;  
 RX MEDLINE=20222556; PubMed=10761919;  
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
 Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
 Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,  
 Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,  
 Rajadaram M.A., Rutherford K.M., Simmonds M., Skelton J.,  
 Whitehead S., Spratt B.G., Barrall B.G.,  
 RT "Complete DNA sequence of a serogroup A strain of Neisseria  
 meningitidis 22491".  
 RL Nature 404:502-506(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MC58 / SEROGROUP B;  
 RX MEDLINE=20175753; PubMed=10710307;  
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
 Eisten J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
 Nelson M.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,  
 Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
 Mason T., Clecio A., Parkey D.S., Blair E., Cline H., Vamathevan J.,  
 Cotton M.D., Uitterback T.R., Khouli H., Qin H., Vamathevan J.,  
 Gill J., Scarlato V., Masigiani V., Piza M., Grand G., Sun L.,  
 Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain  
 MC58".  
 RL Science 287:1809-1815(2000).  
 DR EMBL: AL162754; CAB84026.1;  
 DR EMBL: AE002412; AAF40988.1;  
 DR TIGR: NMB0560;  
 DR InterPro: IPR001451;  
 DR Pfam: PF00132; hexapep. 3.  
 DR PROSITE: PS00101; HEXAPEP\_TRANSFERRASES; 1.  
 DR Transferrase; Acyltransferase.  
 KW KW  
 SQ SEQUENCE 272 AA; 29399 MW; 4CB7AD8A916386EB CRC64;

Query Match 39.6%; Score 649.5; DB 2; Length 272;  
 Best Local Similarity 50.7%; Pred. No. 5.9e-45;  
 Matches 136; Conservative 39; Mismatches 86; Indels 7; Gaps 2;

OY 47 DWIMLEAKSDVKOEPLISNYVYASITSHRSLSALAHILSVKLSNLPNTLELF 106  
 :||:||||: : ||||:| : :||:|  
 Db 12 DLWHTIRETAASAEPLASFLHQTALRHESLSGLAYLHLSKRLSPIDVRLALREIY 71  
 OY 107 ISVLESPELITESTKODLIANKERDPACISVHCFGLGFKGLACQAHRIATLTKOKRKI 166  
 :||:||||: : ||||:| : :||:|  
 Db 72 QOALGSDTQIGKVCADKAIEKRDPADEYSLPLYKGFHAIQAHRIATLRLDGRKT 131  
 OY 167 VALLIONRSESEFADVHFGAKIGKIGLLDHTAVGIGETAVGDNVSIHGVTLGGTGK 226  
 :||:||||: : ||||:| : :||:|  
 Db 132 IATFLONRSEYFVGDVHNAARFGVGMIDHATGTVAAETAVLGNNISILHGVTLGGSGK 191  
 OY 227 QSGDRHPIKIGDVLIGAGSCILGNITIGBGAKIGSGSVVYKVPARTAVGNPARRLIGK 286

Db 192 ECGDRHPIKIGDVGWIGANNSILGNIRIGSNAKIGAGSVVSDVPSTIVGVAPKPAVA-- 249  
 OY 287 ENPRKHDKIPCLTMDQTSYLFEMSDYVI 314  
 Db 250 ----RSLKTPSADMDQNIQFTE-IDPMI 272

## RESULT 14

09KNT2 PRELIMINARY: PRT: 273 AA.  
 AC 09KNT2;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
 DE SERINE ACETYLTRANSFERASE.  
 GN VC2649.  
 OS Vibrio cholerae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J.F., Eissen J.A., Nelson W.C., Cotton R.A., Gwinn M.L.,  
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,  
 McDonald L., Uitterback T., Fleischmann R.D., Newman W.C., White O.,  
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 Fraser C.M.;  
 RT "DNA sequence of both chromosomes of the cholera pathogen vibrio  
 cholerae".  
 RL Nature 406:477-483(2000).  
 DR EMBL: AE004331; AAF95790.1;  
 DR TIGR: VC2649;  
 DR InterPro: IPR001451;  
 DR Pfam: PF00132; hexapep. 4.  
 DR PROSITE: PS00101; HEXAPEP\_TRANSFERRASES; 1.  
 DR Transferrase.  
 KW KW  
 SQ SEQUENCE 273 AA; 29278 MW; 5CBE16376B45B76F CRC64;

Query Match 39.5%; Score 647.5; DB 2; Length 273;  
 Best Local Similarity 50.0%; Pred. No. 8.7e-45;  
 Matches 132; Conservative 50; Mismatches 71; Indels 11; Gaps 3;

OY 39 HQIIEDDDDWIMLEAKSDVKOEPLISNYVYASITSHRSLSALAHILSVKLSNLP 98  
 :||:||||: : ||||:| : :||:|  
 Db 6 HTK-----VQOTVAAERQAEDEPPLASTYATITIKHSLKAAALSYLANLNLAASMP 59  
 OY 99 SNTLELFISVLESPELITESTKODLIANKERDPACISVHCFGLGFKGLACQAHRIAT 158  
 :||:||||: : ||||:| : :||:|  
 Db 60 AMAVREYIEEAFADPSTSEAAACDICTAVNRDPASVMSKPLLYLKGYHALGYSYAVAW 119  
 OY 159 LMKONRKIVALLIONRSESEFADVHFGAKIGKIGLLDHTAVGIGETAVGDNVSIHGVTLGGTGK 218  
 :||:||||: : ||||:| : :||:|  
 Db 120 LMRQKKAATATYFQNOISVACQVDIHHPAARIGRMIDHATGTVIGETAVGDNVSIHGVTLGGTGK 179  
 OY 219 VTLGGTGKSGDRHPIKIGDVGWIGANNSILGNIRIGSNAKIGAGSVVSDVPSTIVGVAPKPAVA 278  
 :||:||||: : ||||:| : :||:|  
 Db 180 VTLGGTGKSGDRHPIKIGDVGWIGANNSILGNIRIGSNAKIGAGSVVSDVPSTIVGVAPKPAVA 239  
 OY 279 PARLIGKSNPRKHXIPCLTMDQ 302  
 :||:||||: : ||||:| : :||:|  
 Db 240 PARIVGRPOS-----DK-PSLMDQ 258  
 RESULT 15  
 09SL28 PRELIMINARY: PRT: 402 AA.  
 ID 09SL28;  
 AC 09SL28;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)



DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE SERINE ACETYLTRANSFERASE.  
GN CSMAT  
OS Cyanidioschyzon merolae.  
OC Eukaryota; Rhodophyta; Bangiophyceae; Cyanidioschyzon.  
OX NCBI\_TaxID=45157;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98288115; PubMed=9622597;  
RA Toda K., Takano H., Miyagishima S., Kuroiwa H., Kuroiwa T.;  
RT "Characterization of a chloroplast isoform of serine acetyltransferase  
from the thermo-acidophilic red alga Cyanidioschyzon merolae.";  
RL Biochim. Biophys. Acta 1403:72-84(1998).  
DR EMBL; AB008428; BAA88412.1; .  
KW Transferase.  
SQ SEQUENCE 402 AA; 43739 MW; D97E69BFF79F452 CRC64;

Query Match 38.4%; Score 629.5; DB 10; Length 402;  
Best Local Similarity 47.1%; Pred. No. 4.3e-43;  
Matches 130; Conservative 51; Mismatches 92; Indels 3; Gaps 2;

OY 27 FRPGSVNRKIHHTQIEDDDVIMLEAKSDVKQEPILSNYYASITSHRSLESALAH 86  
DB 97 FGPVISTVDNV-RTLTYSDDPVMELVREAEIGANEPQLASLYATVLNHRCLEDTLAF 155  
OY 87 ILSVKLSNLNPSNTELFELISVLESEPIESTKODLIANKERDPACISYHCFGLGFKG 146  
DB 156 HIANELASPFQATQYVLFEPDALYODKSYREAIRADLAVARRDPAMKHCVAVLWYSG 215  
OY 147 FLACQAHRIAHITLWKONRKIVALLIONRVSEFAVDIHGAKIGKILIDHATGVIGET 206  
DB 216 YAAIQAYRLAHLWRQDKVLAFLQSEISKCFADVDIHPARISSGVMIDHATGIVIGET 275  
OY 207 AVGDNVSLILGVTLLGIGKSGDRHRKIGDGVILGAGSCLIGNITTEGAKIGSGSVV 266  
DB 276 AVGNDVSLHNTVLLGIGKSGDRHRKIGDGVILGAGSCLIGNITTEGAKIGSGSVV 335  
OY 267 KDVPARTAVGNPARLIGKENPRKHDKIPCLTMDQ 302  
DB 336 KDVPPTIVSGVPAREVYKLSYK--GVYPAFEMDQ 369

Search completed: August 21, 2001, 12:10:05  
Job time: 182 sec